



# Performance Evaluation, Correlation of Traits and Estimation of Heritability and Genetic Advance in Rapeseed (*Brassica Napus*) Genotypes

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**Keywords:** Correlation; Heritability; Genetic advance; Performance and rapeseed genotype.

## Abstract

The improvement of new genotype with better performance than exist variety is one of the point that considered from plant breeder. Twenty three rapeseed genotypes including with two cultivars were evaluated with simple lattice design by two replications with aim to identify genotypes that have high in seed yield performance. The analysis of variance showed that there were significant differences among the tested rapeseed genotypes for days to flowering, days to maturity, number of podplant<sup>-1</sup>, number of seedpod<sup>-1</sup>, thousand seeds weight and seed yieldha<sup>-1</sup> traits. This Indicates variation of genotype performances that shows hopeful for selection. The mean performance of seed yield for rapeseed genotypes in this study indicated that out of twenty three studied genotypes, Eleven genotypes: Sunder-sel-3 (3.248tha<sup>-1</sup>), Sunder-sel-5 (2.991tha<sup>-1</sup>), Dodger Sel.7 (2.763tha<sup>-1</sup>), Sunder-sel-8 (2.751tha<sup>-1</sup>), Belinda sel-7 (2.724tha<sup>-1</sup>), Pura sel -25 (2.529tha<sup>-1</sup>), Axana sel-1 (2.507tha<sup>-1</sup>), Pura sel-19 (2.369tha<sup>-1</sup>), Axana sel-3 (2.364tha<sup>-1</sup>), Buldersel-9 (2.302tha<sup>-1</sup>) and Bulder sel-1(2.245tha<sup>-1</sup>) had higher seed than two standard checks Axana and Swifter. Therefore these genotypes must be considered for next variety performance trial. In addition to this high number of podplant<sup>-1</sup> and number of seedpod<sup>-1</sup> must be considered in order to increase seed yield. Hence they had significant and positive correlated to seed yield performance. High GCV were observed for 1000-SW (78.07%), days to fifty flowering (32.22%) and number of seed pod<sup>-1</sup> (28.61%). High Phenotypic coefficient of variation (PCV) also were observed for number of seed pod<sup>-1</sup>(37.37%) and grain yield (GY) (22.98%). These indicate the existence of considerable genotypic and phenotypic variation among rapeseed genotypes for these traits and greater influence of genetic factors for the expression of these traits, suggesting the possibility of improving these traits through selection. Heritability is a good indicator of transmission of characters from parents to its progeny. High heritability with high Genetic Advance as Percent of Mean (GAM) was recorded for days to flowering (92.72%, 89.94%), seed yieldha<sup>-1</sup>(96.35%, 46.54%), days to maturity (82.68%, 93.47%), number of seed pod<sup>-1</sup>(82.29%, 3296%), number of pod plant<sup>-1</sup> (75.78%, 67.10%), thousand seed weight (57.90%, 30.60%). This high heritability coupled with high genetic advance implied that the trait had governed by additive gene action and selection might be effective for further genetic improvement of this traits.



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## Introduction

Rapeseed (*Brassica napus* L.) is the world's second produced oilseed and accounts for nearly 12% of world major vegetable oil production [1]. Rape seed is an essential oilseed crop which used in many different areas as an edible oil, biodiesel, lubricant, and feed. It is one of the most popular oil crops in Europe where about 63% of oilseeds production in 2017 [2]. Brassica crops may be among the oldest cultivated plants known to humans. The four most widely cultivated species of Brassica: *B. juncea*, *B. napus*, *B. oleracea* and *B. rapa*, are highly polymorphic. A theory about the evolution and relationships between members of the plant genus brassica, developed and first published in 1935 by Woo Jang-choon, a Korean botanist, who made synthetic hybrids between the diploid and tetraploid species and examined how the chromosomes paired in the resulting triploids. The theory is based on the idea that the genomes of three ancestral species of brassica combined in various configurations to create three of the common contemporary vegetables and oilseed crop species. The theory has confirmed that genomic duplication may have preceded the divergence of the cultivated brassica from one another [3].

*Brassica napus* has probably developed in the area where the wild forms of its ancestral species are sympatric, in the Mediterranean area. 25 Wild forms of *Brassica napus* are unknown, so it is possible it originated in cultivation, and the production of oilseed brassica napus probably started in Europe during the Middle Age [4]. Rapeseed related to mustard, cabbage, broccoli, cauliflower and turnip. Rapeseed (*Brassica napus* var. *napus*) is an annual oil crop in brassica family. It is also known as rape and oilseed rape. Rapeseed plants grow from three to five feet tall and have yellow flowers with four petals. It has a deep taproot and fibrous, near-surface root system [5].

Rapeseed also used as a feed especially rapeseed meal and rapeseed cake, which are by-products of oil [6]. Rapeseed feeds contain more mineral ingredients (calcium, iron, manganese, phosphorus, magnesium, and selenium) than soybean meal [7]. Rapeseed is globally known as a huge source of valuable nutrients. A significant advantage of rapeseed oil is that it is rich in unsaturated fatty acids. Thus, rapeseed oil has health-promoting effects on diabetes, metabolic syndrome, and type 2 diabetes [8].

In Ethiopia, the rapeseed research started in late 1960s in Institute of Agricultural Research/IAR/ by introducing materials from Canada and West Germany with wide objective of breeding to develop high yielding varieties of good nutritional value [6]. The state started production in large-scale farms. But due to Black leg diseases (*Leptosphaeria maculans*) production of the crop obstructed in late 1980 [6]. To improve this problem and bring up the rapeseed crop back into production and improvement evaluation for yield and yield related traits for releasing varieties with high seed is very important. Therefore the present experiment was conducted in order to evaluate the agronomic performance of available rapeseed genotypes. Looking only the performance of genotypes for yield is not effective to select genotypes which could be used as a parent material for further improvement activities since yield is influenced by different factors. Hence when performing variability activities, it is also recommended to look on the existence of variation

for other yield attributing traits such as productive tiller, filled grain, maturity date, biomass yield, thousand grain weight, and plant height in order to use them as indirect selection criteria [9]. The success of crop breeding programs mainly depends on the existence of genetic variation and the inheritance of traits of interest. Analysis of genetic variation assists the breeder to decide the proper strategy and selection criteria to be used for the improvement of the target traits. Genetic variability is a measure of the tendency of individual genotypes in a population to vary from one another. Genetic variability in a population is important for biodiversity because without variability, it becomes difficult for a population to adapt to environmental changes and therefore makes it more prone to extinction and genetic variation and mode of inheritance of quantitative and qualitative traits are of prime importance in planning the breeding programme [10]. Assessment of variability for yield and other characters becomes absolutely essential before planning for an appropriate breeding strategy for genetic improvement [11].

## Materials and methods

### Experimental Site

The study was conducted at Kulumsa during the 2020/21 cropping season, Kulumsa which found in Arsi Zone of Oromia Regional State, is located at 8° 01' N latitude and 39° 09' E longitude within an altitude of 2200 m. a. s. l. The soil type of the area is clay soil with soil composition of 63.123% clay, 28.125% silt and 8, 75% sand soil. The pH of the soil is relatively acidic which 6.08. The maximum and minimum annual temperature of the area were 22.8°C and 12.14°C with 8737mm of annual rainfall in the Table 2 as follows (weather data Source: Kulumsa Agricultural research Center during the 2020 cropping season).

**Table 1:** Monthly Average of rainfall and Temperature during 2020/21 Cropping Season.

Month	2020			2021		
	Rain	Tmax	Tmin	Rain	Tmax	Tmin
Jan	8.8	23.6	11.2	0.0	23.9	9.3
Feb	3.9	25.5	11.2	7.6	24.6	11.3
Mar	68.4	26.4	13.4	0.4	26.8	12.3
Apr	104.6	26.2	12.9	66.0	26.4	13.0
May	94.7	24.9	12.9	124.5	24.8	11.8
Jun	123.7	23.8	12.9	59.9	24.2	12.0
Jul	251.4	21.2	13	170.6	20.6	13.0
Aug	143.5	21.2	12.9	121.9	21.3	12.7
Sep	130.8	28.1	12.2	191.2	20.9	11.2
Oct	64	24	12.8	63.7	22.8	12.6
Nov	1	23.5	12.2	6	23.7	11.1
Dec	0.2	23	10.7	0	29.6	9.2

### Experimental Materials.

Twenty three (23) rapeseed genotypes were planted and evaluated at kulumsa Agricultural Research Center site with two standard checks; which was obtained from Holeta Agricultural Research Center shown in the (Table 2).

**Table 2:** Plant materials used for the study.

SrNO	Name of Genotypes	Crop Type	Source
1	Dodger Sel.7	Rapeseed	HARC
2	Sunder-sel-3	Rapeseed	HARC
3	Sunder-sel-5	Rapeseed	HARC
4	Sunder-sel-8	Rapeseed	HARC
5	Sunder-sel-9	Rapeseed	HARC
6	Axana sel-1	Rapeseed	HARC
7	Axana sel-3	Rapeseed	HARC
8	Belinda sel-3	Rapeseed	HARC
9	Belinda sel-7	Rapeseed	HARC
10	Belinda sel-9	Rapeseed	HARC
11	Bulder sel-1	Rapeseed	HARC
12	Bulder sel-4	Rapeseed	HARC
13	Bulder sel-6	Rapeseed	HARC
14	Bulder sel-8	Rapeseed	HARC
15	Bulder sel-9	Rapeseed	HARC
16	Pura sel-1	Rapeseed	HARC
17	Pura sel-3	Rapeseed	HARC
18	Pura sel- 5	Rapeseed	HARC
19	pura sel -6	Rapeseed	HARC
20	Pura sel- 7	Rapeseed	HARC
21	pura sel-19	Rapeseed	HARC
22	pura sel -20	Rapeseed	HARC
23	pura sel -25	Rapeseed	HARC
24	Axana	Rapeseed	HARC
25	swifter	Rapeseed	HARC

### Experimental Design and Trial Management

The treatments were laid out in simple 5x5 lattice design with two replications having plot size of 5.4m<sup>2</sup>(1.8m\*3m), Accommodating 6 rows of 3m length. The spacing between rows and plants was 0.3cm and 0.1cm. The seed rate and fertilizer rate used was 10kg/ha and 23/23kg/ha of N/P<sup>2</sup>O<sup>5</sup> respectively. Agronomic practices such the land tillage was prepared by tractor three times and two hand weeding were applied to the crop during experiment.

### Data Collection

The following experimental data were collected for the studied traits of rapeseed genotypes:

**Days to flowering (DF):** Days that was taken to reach 50% flowering was recorded by counting the days it takes to flower from sowing date.

**Days to maturity (DM):** This was the day when above 90% of the pods in the plot matured, and it was recorded as the time of maturity for each plot.

**Plant Height (PH):** Plant height was measured immediately after plants stop growing (when the plants on the plot showing 80% maturity).

**Stand Count (STC):** Were recorded on plot based two weeks after emergence in order to check the establishing the number of plants in a plot and comparing it with the expected crop numbers, whereas plant population records only numbers. It allows to determine germination rate, and plant health. They are

based on visual inspection and plant calculation on plot/on small pre-defined field areas.

**Number of podsplant<sup>-1</sup> (NPPP):** Taking five plants as a sample from a plot, numbers of pods plant<sup>-1</sup> were counted and the mean average numbers of pods were computed and taken as representative of the plot, specifically genotype.

**Number of Seedpod<sup>-1</sup> (NSPP):** Taking five plants as a sample from a plot and five randomly selected numbers of pods taken from the plant then seedpod<sup>-1</sup> were counted and the mean average numbers of seeds were computed and taken as representative of the pods, specifically genotype.

**Thousand Seed Weight (TSW):** Thousand seed weight was conducted by weighing randomly selected 1000 seed. It is directly/positively correlated with seed size, i.e, the higher the weight of thousand seeds, the larger the size of individual seeds of that genotype. This is necessary to know the plants died and unable to reach for harvesting due to adverse effects of environment at 7% moisture content.

**Grain yield per plot (GY):** Grain yield per plot was measured in order to know the exact weight of yieldplot<sup>-1</sup>.

### Data analysis

The measured data for each parameters were subjected to Analysis Of Variance (ANOVA) for simple lattice design by using PROC GLM of SAS Software version 9.0 [12]. Duncan's Multiple Rang Test (DMRT) was used for means separation.

Correlation of quantitative traits were measured to identify dependance, meaning statistical relationship between variables or observed

data values. In this study the correlation was done by SAS PROC CORR Method to illustrate statistical relationships among the studied traits of rapeseed genotypes.

Genotypic variance ( $\sigma^2g$ ), phenotypic variance ( $\sigma^2p$ ), Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV) were estimated using the formula adopted from [13]:

$$\text{Environmental variance } (\sigma^2e) = \text{EMS, Genotypic variances } (\sigma^2g) = \frac{\text{GMS} - \text{EMS}}{r},$$

Phenotypic Variance ( $\sigma^2P$ ) =  $\sigma^2g + \sigma^2e$  Where, GMS = Genotypic mean square, and EMS = Error mean square, From the ANOVA respectively. r is number of replications.

Coefficient of variation of variation at genotypic and phenotypic levels were estimated using the following formula.

$$\text{Genotypic Coefficient of Variation (GCV)} = (\sqrt{\sigma^2g} / \text{grand mean}) * 100$$

$$\text{Phenotypic Coefficient of Variation (PCV)} = (\sqrt{\sigma^2p} / \text{grand mean}) * 100,$$

### Results and Discussions

Analysis of variance obtained from eight studied traits of rapeseed genotypes were indicated in (Table 3). The analysis of variance showed that there were significant ( $P \leq 0.01$ ) differences among the tested rapeseed genotypes for days to flowering, days to maturity, number of pod plant<sup>-1</sup>, number of seed pod<sup>-1</sup>, thousand seeds weight and seed yield ha<sup>-1</sup> traits. The result correspondent with the report of [14] except for days to flowering,

**Table 3:** Indicates analysis of variance for eight studied traits of rapeseed genotypes.

Source of variation	d/f	Mean squares of Traits							
		DF	DM	PHT	STC	NPP	NSPP	TSW	GY
Genotype	24	8.28 **	40.81 **	100.80	29.80	2193.78**	8.27 **	0.55 **	265691.34 **
Block	9	5.20	18.81	164.22	19.98	788.06	9.70	0.44	297544.07
Error	16	0.65	8.55	145.67	22.48	701.28	1.78	0.40	10068.17

NB: \*\*: Significant; d/f: Degree of freedom; DF: days of 50% flowering; DM: Days of 90% maturity; PHT: Plant height; STC: Stand count; NPP: Number of pod plant<sup>-1</sup>; NSP: Number of seed pod<sup>-1</sup>; TWS/1000: Thousand seed weight and GY: Seed yieldtha<sup>-1</sup>.

days to maturity and plant height. This indicates the existence of variability among the genotypes tested that is important for selection and breeding program.

### Mean performance and Range

The mean performance of the studied rapeseed genotypes were presented in the (Table 4). Among the tested genotypes the maximum seed yield than standard checks Axana and Swifter were recorded for Sunder-sel-3 (3.248tha<sup>-1</sup>), Sunder-sel-5 (2.991tha<sup>-1</sup>), Dodger Sel.7 (2.763tha<sup>-1</sup>), Sunder-sel-8 (2.751tha<sup>-1</sup>), Belinda sel-7 (2.724tha<sup>-1</sup>), pura sel-25 (2.529tha<sup>-1</sup>), Axana sel-1 (2.507tha<sup>-1</sup>), pura sel-19 (2.369tha<sup>-1</sup>), Axana sel-3 (2.364tha<sup>-1</sup>), Buldersel-9 (2.302tha<sup>-1</sup>) and Bulder sel-1(2.245tha<sup>-1</sup>). The minimum seed yield was also recorded for the genotype Belinda sel-9 (1.358 tha<sup>-1</sup>) (Table 4). The mean value of the 11 (44%) genotypes tested for this study had shown maximum seed yield than the grand mean and standard checks of the tested genotypes.

The maximum number of podplant<sup>-1</sup> was recorded for the genotype Sunder sel-3 (245) and the minimum number of podplant<sup>-1</sup> was recorded for genotype Blinda sel-1 (102). While the mean value performance of number of podplant<sup>-1</sup> was 144. The result was similar with findings of [15] who observed the Number of siliqua (pod) plant<sup>-1</sup> ranged from 90.64 to 246.53. The findings also similar with the [16,17] who reported that the number of siliqua plant<sup>-1</sup> for different lines and varieties of

B. rapa. Similarly among the tested genotypes, the maximum number of seedpod<sup>-1</sup> were recorded for genotypes: Sunder sel-3 (24), Sunder sel-8 (22), Builder sel-8 (21) and Pura sel-6 (21) ranked first, second and third in seed pod<sup>-1</sup>, respectively in (Table 4). This indicated that different genotypes of rapeseed had different range of seed pod<sup>-1</sup>. The result was agreed with [16,17] found that the seed siliqua<sup>-1</sup>(seed pod<sup>-1</sup>) for different lines and varieties of B. rapa ranged from 11.98 to 16.22 and 12.83 to 20.87 respectively.

Significant variation in days to fifty flowering and days to maturity had observed which ranged from 61 days to 69 days and 135 days to 149 days respectively Table (3). Days to 50% flowering was maximum in Bulder sel-1, and Bulder sel-8 (69 days) and the minimum Pura sel-3 (61days) while days to maturity was maximum in Swifter (149 days) and the minimum in Pura sel-19 (135 days). The result matched with the findings of [15-17] Variability and heritability study in rapeseed 109.

A Plant height ranged from 134cm to 163cm. The highest plant height was recorded in Bulder sel-8(163cm) and lowest in Axana (134cm) genotypes (Table 4). The result differed from the findings of [13-15] who reported that, the plant height for different lines and varieties of B. rapa ranged from 67.86 cm to 149.23 cm, 80.77 to 111.47 cm and 94.56 to 107.73 cm respectively. This might be due to environmental effects.

**Table 4:** Mean performance of tested rapeseed genotypes traits.

Treatment Code	Genotypes	DF	DM	PHT	STC	NPP	NSPP	TSW	GY
1	Dodger Sel.7	68	144	140	79	187	21	6	2.763
2	Sunder-sel-3	67	145	158	89	245	24	6	3.248
3	Sunder-sel-5	67	145	153	89	159	20	6	2.991
4	Sunder-sel-8	67	141	155	90	235	22	6	2.751
5	Sunder-sel-9	67	138	143	92	133	17	6	2.263
6	Axana sel-1	68	148	155	89	142	18	4	2.507
7	Axana sel-3	66	139	143	93	125	16	5	2.364
8	Belinda sel-3	66	142	158	92	135	17	5	2.201
9	Belinda sel-7	62	135	145	97	184	18	6	2.724
10	Belinda sel-9	67	135	153	92	140	18	6	1.358
11	Bulder sel-1	69	145	148	82	102	18	6	2.245
12	Bulder sel-4	68	143	150	93	230	18	5	1.948
13	Bulder sel-6	66	145	155	93	120	21	5	1.974
14	Bulder sel-8	69	145	158	92	148	16	5	1.465
15	Bulder sel-9	63	137	163	92	124	20	6	2.302
16	Pura sel-1	66	136	158	85	105	20	5	2.126
17	Pura sel-3	61	135	143	92	121	18	5	1.931
18	Pura sel-5	65	135	155	91	110	16	6	2.177

19	pura sel -6	68	145	148	80	131	21	6	2.030
20	Pura sel- 7	66	144	155	90	153	19	5	2.026
21	pura sel-19	64	134	153	88	122	13	5	2.369
22	pura sel -20	68	141	163	88	110	15	6	2.229
23	pura sel -25	63	136	158	88	119	17	6	2.529
24	Axana	67	147	138	93	117	17	5	2.329
25	swifter	68	149	140	96	114	15	5	2.275
Mean		66	141	151	90	144	18	5	2.285
CV		1.23	2.10	8.0	5.30	18.37	7.37	0.6	24.31
LSD		1.71	6.20	25.59	10.051	56.139	2.831	0.2	1043

NB CV: Coefficient of variation; LSD: Least significant different; DF: days of 50% flowering; DM: Days of 90% maturity; PHT: Plant height; STC: Stand count; NPP: Number of pod plant<sup>-1</sup>; NSP: Number of seeds pod<sup>-1</sup>; TWS: Thousand seed weight and GY: Seed yield/ grain yield.

**Table 5:** Correlation coefficients for eight characters of rapeseed genotypes.

Traits	DF	DM	PHT	stand	NPP	NSPP	TSW
DF	1						
DM	0.59439**	1					
PHT	-0.15443	-0.1644	1				
STC	-0.26935	0.01327	-0.0134	1			
NPP	0.1408	0.17195	0.07178	0.09321	1		
NSPP	0.09517	0.24185	0.09963	-0.12857	0.47**	1	
TSW	0.09058	-0.04996	0.07725	-0.31	0.37**	0.5287	1
GY	-0.17534	-0.00128	-0.05663	0.01533	0.42**	0.21*	0.2385

### Correlation of the Traits

The results of correlation analysis of seed yield and yield related components and between seed yield is presented in (Table 5). Correlation coefficient analysis for seed yield indicated that seed yield is significant and positive correlated with number of pod plant<sup>-1</sup> ( $r=0.47$ ) and number of seedpod<sup>-1</sup> ( $r=0.21$ ) in the (Table 5). Similarly the number of seedpod<sup>-1</sup> is significant and positive correlated with number of podplant<sup>-1</sup> ( $r=0.47$ ) and also the number seed weight not significant and positive correlated with number of podplant<sup>-1</sup>. Days to maturity is significant and highly positive correlated with days to fifty flowering as shown in (Table 5).

Correlation coefficient analysis for seed yield indicated that seed yield is significant and positive correlated with number of podplant<sup>-1</sup> ( $r=0.42$ ) and number of seedpod<sup>-1</sup> ( $r=0.21$ ). This gain is similar with findings of [18,19] research report. Similarly the number of seedpod<sup>-1</sup> is significant and positive correlated with number of podplant<sup>-1</sup> ( $r=0.47$ ) this findings also correspondent with [18,19] findings. The number of seed weight not significant and positive correlated with number of pod plant<sup>-1</sup>. This findings is not correspondent with [18] findings. Days to maturity is significant and highly positive correlated with days to fifty flowering as shown in (Table 5). This findings also correspondent with [18] report.

### Estimation of genetic parameters

The estimates of genotypic ( $\sigma^2_g$ ) and phenotypic ( $\sigma^2_p$ ) variances, phenotypic (PCV) and genotypic (GCV) coefficients of variation, heritability (broad sense), genetic advance and genetic advance as percent of mean were determined for the traits considered and are presented in Table 6.

### Phenotypic and genotypic coefficients of variation

PCV and GCV values greater than 20% are considered as high, values between 10% and 20% as medium and values less than 10% as low, According to [20]. High GCV were observed for 1000-SW (78.07%), days to fifty flowering (32.22%), number of seed pod<sup>-1</sup> (28.61%) according to the concept of [20]. Similar result were reported by [21] for number of seedpod<sup>-1</sup>. These indicate the existence of phenotypic variation among the genotypes considered in the present study and the possibility of genetic improvement of those traits through selection. Medium GCV was observed for traits like Grain Yield (GY) (18.69%) and number of podplant<sup>-1</sup> (16%) and days to maturity (12.94%). Low GCV value observed for plant height (4.07%) and stand count (10.44%). The low GCV estimates observed in this investigation indicate the presence of narrow genetic variation on the traits and greater influence of environmental factors for the expression of these traits. High Phenotypic Coefficient of Variation (PCV) were observed for number of seed pod<sup>-1</sup> (37.37%) and Grain Yield (GY) (22.98%). These results indicate the existence of considerable genotypic variability among rapeseed genotypes for these traits and greater influence of genetic factors for the expression of these traits, suggesting the possibility of improving these traits through selection. Medium PCV was observed for traits like 1000-SW (19.49%) and number of seed pod<sup>-1</sup> (17.61%). Indicating the existence of small phenotypic variability among the rapeseed genotypes for these traits. In the this study, low PCV was observed for days to fifty flowering, days to maturity, plant height and stand count which indicate the presence of narrow genetic variation. However, the improvement of this trait could be possible through hybridization followed by selection.

### Estimate of Heritability and Genetic Advance

Heritability is a good indicator of transmission of charac-

ters from parents to its progeny. Dabholkar generally classified heritability estimates as low (5-10%), medium (10-30%) and high (30-60%) [22]. The estimates of heritability help the plant breeder in selection of genotypes from diverse genetic population. Therefore, high heritability helps in effective selection for a particular character. All of the traits in this study were manifested high according to dabholkar classification. That is ranged from (40.90%-96.35%). The highest broad sense heritability value manifested for seed/grain yield $ha^{-1}$  (GY) (96.35%) followed by days of fifty flowering (92.721%), days of maturity (82.68%) and number of seed pod $^{-1}$  (82.29%), number of pod plant $^{-1}$  (75.78%) respectively in the (Table 6). This high heritability indicates that selection will be effective.

This result similar with the report of [23].

**Table 6:** Shows Estimation of Variability of Rapeseed Genotypic Traits under Study.

Triats	( $\sigma_2g$ )	( $\sigma_2e$ )	( $\sigma_2p$ )	gcv	pcv	H2	GA	GAM
DF	8.28	0.65	8.93	32.22	4.53	92.72	59.36	89.94
DM	40.81	8.55	49.36	12.94	4.98	82.68	131.79	93.47
PHT	100.8	145.67	246.47	4.07	10.40	40.90	207.12	13.72
STC	29.8	22.48	52.28	10.44	8.03	57.00	112.62	12.51
NPP	2193.78	701.28	289.506	16.18	37.37	75.78	966.26	67.10
NSPP	8.27	1.78	10.05	28.61	17.61	82.29	59.33	32.96
TSW	0.55	0.4	0.95	78.07	19.49	57.89	153.00	30.60
GY	265.69134	100.68	275.76	18.69	22.98	96.35	1063.38	46.54

The genetic advance is a valuable indicator of the progress that could be achieved as a result of selecting the relevant population [24]. In this study, there is no trait which can be categorized as trait low genetic advance. Moderate genetic advance as percent of the mean was recorded by plant height 12.51% and stand count 13.72%. Moderate GAM indicated that moderate action of both additive and non-additive genes on the control of those characteristics. However, In this study high GAM was recorded for days to maturity (93.94%), days of flowering (89.94%), number of pod plant $^{-1}$  (67.10%), grain yield $ha^{-1}$  (46.54%), number of seedpod $^{-1}$  (32.96%), thousands seed weight (30.60%) in (Table 6). This high GAM indicated that the maximum control of characters by additive gene action and the high possibility of using this trait for genetic improvement through selection. Knowledge of heritability coupled with genetic advance could be more beneficial than knowing only heritability of characters [25]. In this study, high heritability with high GAM was recorded for days to flowering (92.72%, 89.94%), seed yield  $ha^{-1}$  (96.35%, 46.54%), days to maturity (82.68%, 93.47%), number of seed pod $^{-1}$  (82.29%, 3296%), number of pod plant $^{-1}$  (75.78%, 67.10%), thousand seed weight (57.90%, 30.60%). The result was similar with the observed report by [26,27]. This high heritability coupled with high genetic advance implied that this trait had governed by additive gene action and selection might be effective for further genetic improvement of this trait.

### Conclusion

The analysis of variance showed that there were significant differences among the tested rapeseed genotypes for days to flowering, days to maturity, number of pod plant $^{-1}$ , number of seed pod $^{-1}$ , thousand seeds weight and seed yield $ha^{-1}$  traits. This indicates the existence of variability among the genotypes tested that is important for selection to the next breeding plan. Among the tested genotypes the maximum seed yield

than standard checks Axana and Swifter were recorded for genotypes: Sunder-sel-3 (3.248 $tha^{-1}$ ), Sunder-sel-5 (2.991 $tha^{-1}$ ), Dodger Sel.7 (2.763 $tha^{-1}$ ), Sunder-sel-8 (2.751 $tha^{-1}$ ), Belinda sel-7 (2.724 $tha^{-1}$ ), pura sel -25 (2.529 $tha^{-1}$ ), Axana sel-1 (2.507 $tha^{-1}$ ), Pura sel-19 (2.369 $tha^{-1}$ ), Axana sel-3 (2.364 $tha^{-1}$ ), Buldersel-9 (2.302 $tha^{-1}$ ) and Bulder sel-1(2.245 $tha^{-1}$ ). These eleven genotypes should be chosen for next variety performance trails. Correlation coefficient analysis for seed yield indicated that seed yield is significant and positive correlated with number of pod plant $^{-1}$  ( $r=0.47$ ) and number of seedpod $^{-1}$  ( $r=0.21$ ). Similarly the number of seedpod $^{-1}$  is significant and positive correlated with number of pod plant $^{-1}$  ( $r=0.47$ ). These triats should be considered hence they had significant and positive correlated to seed yield performance. The improvement of new genotype with better performance than exist variety is one of the point that considered from plant breeder. Twenty three rapeseed genotypes including with two cultivars were evaluated with simple lattice design by two replications with aim to identify genotypes that have high in seed yield performance. The analysis of variance showed that there were significant differences among the tested rapeseed genotypes for days to flowering, days to maturity, number of podplant $^{-1}$ , number of seedpod $^{-1}$ , thousand seeds weight and seed yield $ha^{-1}$  traits. This Indicates variation of genotype performances that shows hopeful for selection. The mean performance of seed yield for rapeseed genotypes in this study indicated that out of twenty three studied genotypes, Eleven genotypes: Sunder-sel-3 (3.248 $tha^{-1}$ ), Sunder-sel-5 (2.991 $tha^{-1}$ ), Dodger Sel.7 (2.763 $tha^{-1}$ ), Sunder-sel-8 (2.751 $tha^{-1}$ ), Belinda sel-7 (2.724 $tha^{-1}$ ), Pura sel -25 (2.529 $tha^{-1}$ ), Axana sel-1 (2.507 $tha^{-1}$ ), Pura sel-19 (2.369 $tha^{-1}$ ), Axana sel-3 (2.364 $tha^{-1}$ ), Buldersel-9 (2.302 $tha^{-1}$ ) and Bulder sel-1(2.245 $tha^{-1}$ ) had higher seed than two standard checks Axana and Swifter. Therefore these genotypes must be considered for next variety performance trial. In addition to this high number of podplant $^{-1}$  and number of seedpod $^{-1}$  must be considered in order to increase seed yield. Hence they had significant and positive correlated to seed yield performance.

High GCV were observed for 1000-SW(78.07%), days to fifty flowering (32.22%) and number of seed pod $^{-1}$  (28.61%). These indicate the existence of phenotypic variation among the genotypes considered in the present study and the possibility of genetic improvement of those traits through selection. High Phenotypic Coefficient of Variation (PCV) also were observed for number of seed pod $^{-1}$  (37.37%) and grain yield (GY) (22.98%). These results indicate the existence of considerable genotypic variability among rapeseed genotypes for these traits and greater influence of genetic factors for the expression of these traits.

Heritability is a good indicator of transmission of characters from parents to its progeny. High heritability with high genetic advance as percent of mean (GAM) was recorded for days to flowering (92.72%, 89.94%), seed yield $ha^{-1}$  (96.35%, 46.54%), days to maturity (82.68%, 93.47%), number of seed pod $^{-1}$  (82.29%, 3296%), number of pod plant $^{-1}$  (75.78%, 67.10%), thousand seed weight (57.90%, 30.60%). This high heritability coupled with high genetic advance implied that the trait had governed by additive gene action and selection might be effective for further genetic improvement of this traits. Heritability is a good indicator of transmission of characters from parents to its progeny. High heritability with high genetic advance as percent of mean (GAM) was recorded for days to flowering (92.72%, 89.94%), grain yield $ha^{-1}$  (96.35%, 46.54%), days to maturity (82.68%, 93.47%), number of seedpod $^{-1}$  (82.29%, 3296%),

number of pod plant<sup>1</sup> (75.78%, 67.10%), thousand seed weight (57.90%, 30.60%). This high heritability coupled with high genetic advance implied that this trait had governed by additive gene action and selection might be effective for further genetic improvement of this traits.

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